

WHY R?

BY MORTEZA SABRI

2020-02-09



A screenshot of a MacBook Pro laptop displaying a code editor window for a PHP file named 'functions.php'. The code is part of a plugin for WordPress, specifically for extended registration. It includes functions for loading templates, handling registration forms, and validating user input. The editor shows syntax highlighting for PHP and comments. The status bar at the bottom indicates it's a MacBook Pro.

```
public_html >
    > cert
    > cgi-bin
    > phpmyadmin
    > wp-admin
    > wp-content
        > languages
        > plugins
            > acf-accordion
            > advanced-custom-fields-pro
            > amr-shortcode-any-widget
            > charitable
            > charitable-ambassadors
            > charitable-anonymous
            > charitable-license-tester
            > charitable-user-avatar
            > contact-form-7
            > contact-form-7-to-database-extension
            > custom-registration-form-builder-with-submissi...
            > disable-comments
            > extended-registration
                > backend
                > classes
                > js
                > views
                > debug.php
                > extended-registration.php
                    functions.php
                > LayerSlider
                > really-simple-captcha
                > regenerate-thumbnails
                > relative-image-urls
Projects
```

```
functions.php * X
75 include($view_path . 'header.php');
76 $fields = ER_Model::factory('Field')->loadTemplates();
77 foreach ($fields as $field) {
78     er_render_field($field);
79 }
80
81 include($view_path . 'footer.php');
82 }
83
84
85 function er_handle_registration_form() {
86     $results = array('errors'=>array());
87     $password = null;
88     $username = null;
89     $usernameField = er_option('er_username_field');
90     $passwordField = er_option('er_password_field');
91
92     # Create new registration
93     $registration = ER_Model::factory('Registration');
94     $registration['time'] = date('Y-m-d H-i-s');
95
96     $fields = ER_Model::factory('Field')->loadTemplates();
97     foreach ($fields as $field) {
98         $field['template_id'] = $field['id'];
99         $field['id'] = null;
100
101         # Assign value and validate
102         switch ($field['type']) {
103             case 'title':
104             case 'description':
105                 continue;
106                 break;
107
108             case 'checkbox':
109                 $field['value'] = isset($_POST[$field['unique_name']]);
110                 if ($field['required'] && !$field['value'])
111                     $results['errors'][$field['unique_name']] = 'Vous devez cocher ce champ';
112                 break;
113
114             case 'email':
115                 $field['value'] = safe_get($_POST, $field['unique_name']);
116                 if ($field['required'] && !$field['value'])
117                     $results['errors'][$field['unique_name']] = 'Veuillez entrer une adresse e-mail valide';
118                 elseif (!filter_var($field['value'], FILTER_VALIDATE_EMAIL))
119                     $results['errors'][$field['unique_name']] = 'L\'adresse e-mail que vous avez entrée n\'est pas valide';
120                 break;
121
122             case 'password':
123                 break;
124         }
125     }
126 }
```



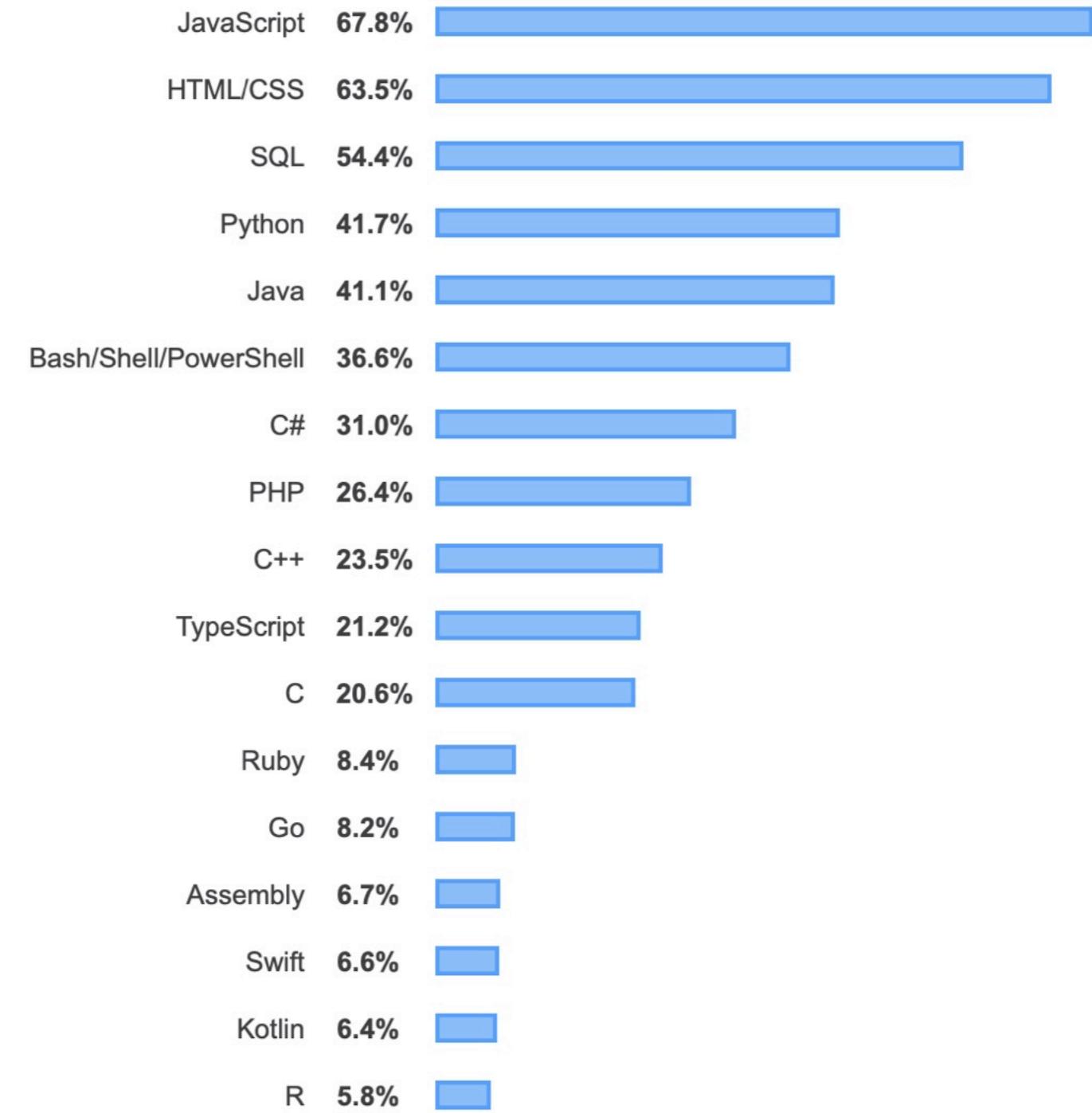
SYLLABUS

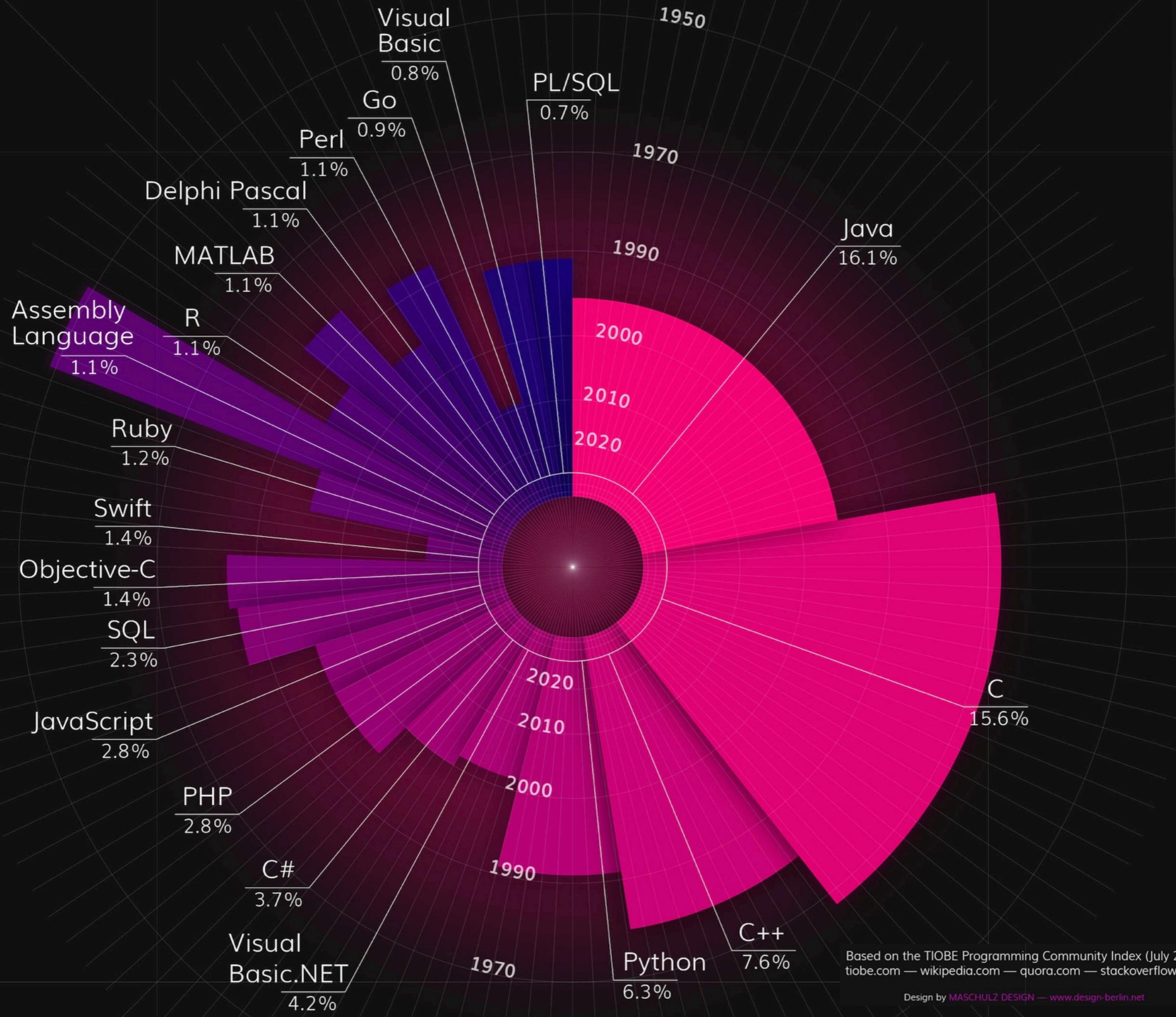
- ▶ Overview of Programming Languages
- ▶ Why R?
- ▶ What can R do in Biology?
- ▶ R applications in Data Science
- ▶ Live Demo:
 - ▶ qRT-PCR
 - ▶ microarray
 - ▶ RNA-seq
- ▶ Discussion and Conclusion

TIOBE INDEX FOR FEBRUARY 2020

Feb 2020	Feb 2019	Change	Programming Language	Ratings	Change
1	1		Java	17.358%	+1.48%
2	2		C	16.766%	+4.34%
3	3		Python	9.345%	+1.77%
4	4		C++	6.164%	-1.28%
5	7	▲	C#	5.927%	+3.08%
6	5	▼	Visual Basic .NET	5.862%	-1.23%
7	6	▼	JavaScript	2.060%	-0.79%
8	8		PHP	2.018%	-0.25%
9	9		SQL	1.526%	-0.37%
10	20	▲	Swift	1.460%	+0.54%
11	18	▲	Go	1.131%	+0.17%
12	11	▼	Assembly language	1.111%	-0.27%
13	15	▲	R	1.005%	-0.04%

DEVELOPER SURVEY RESULTS 2019





Based on the TIOBE Programming Community Index (July 2018)
tiobe.com — wikipedia.com — quora.com — stackoverflow.com

Design by MASCHULZ DESIGN — www.design-berlin.net

WHAT CAN PROGRAMMING DO?

Are You  Kidding Now?

EVERYBODY IN THIS COUNTRY
SHOULD LEARN HOW TO PROGRAM A
COMPUTER... BECAUSE IT TEACHES
YOU HOW TO THINK

Steve Jobs

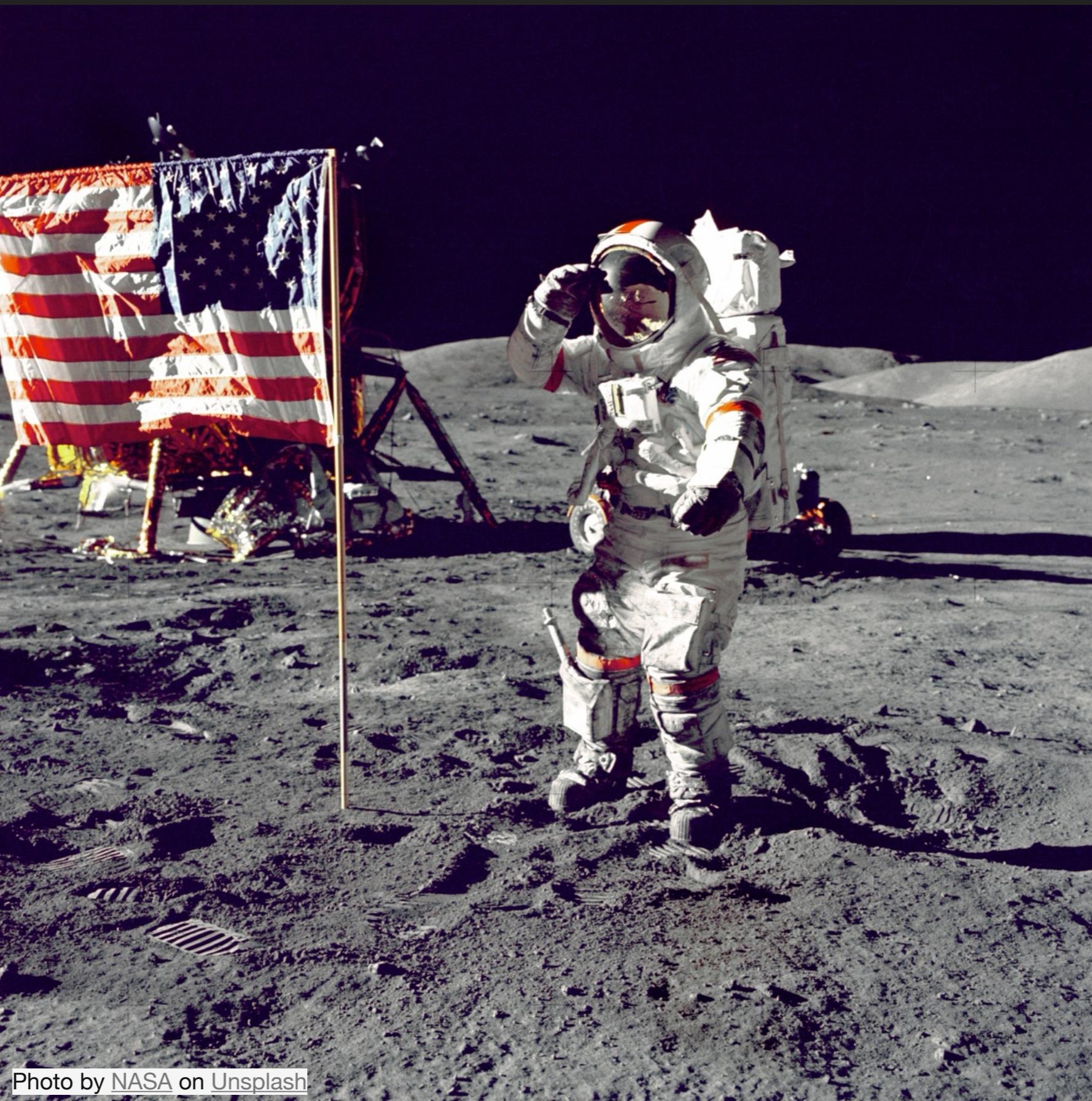


Photo by [NASA](#) on [Unsplash](#)

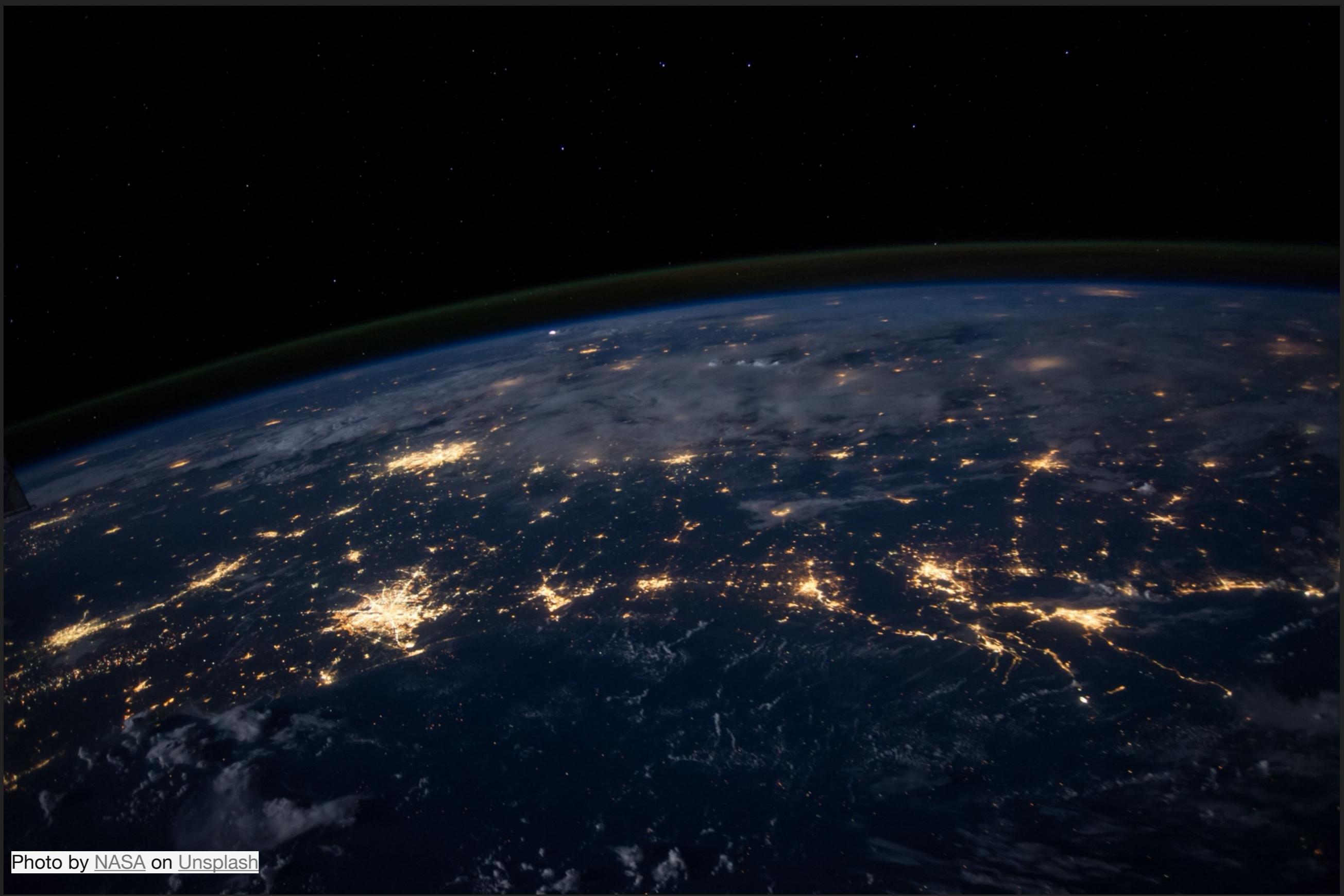
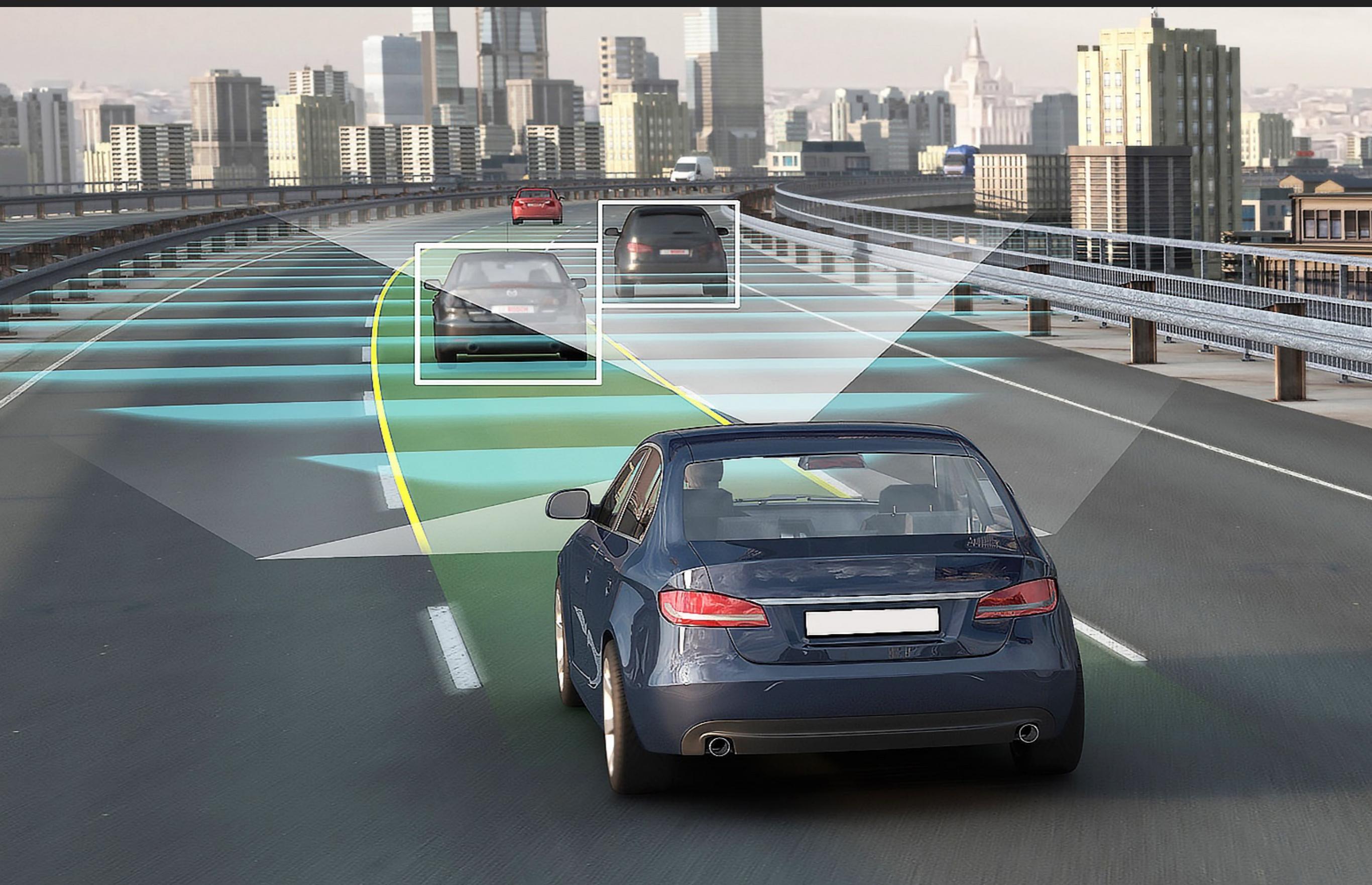


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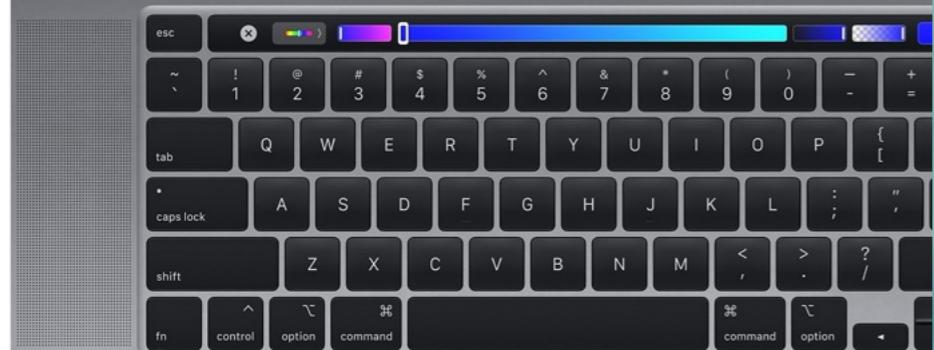












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#3 REASONS WHY EVERYONE SHOULD LEARN PROGRAMMING

- ▶ Coding develops structured and creative thinking
- ▶ Programming makes things easier for you
- ▶ Learning to program teaches you persistence



AN ADVENTURE TOO BIG FOR THE REAL WORLD



A STEVEN SPIELBERG FILM
**READY
PLAYER
ONE**

MUSIC BY ALAN SILVESTRI EXECUTIVE PRODUCERS ADAM SOMNER DANIEL LUPI
CHRIS DEFARIA AND BRUCE BERMAN BASED ON THE NOVEL BY ERNEST CLINE
SCREENPLAY BY ZAK PENN AND ERNEST CLINE PRODUCED BY DONALD DE LINE, p.g.a.
KRISTIE MACOSKO KRIEGER, p.g.a. STEVEN SPIELBERG, p.g.a. DAN FARAH, p.g.a.
DIRECTED BY STEVEN SPIELBERG

PG-13
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AN ADVENTURE TOO BIG FOR THE REAL WORLD



18

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R CAN FACILITATE REPRODUCIBLE RESEARCH

Dr Jessica Hedge is a Postdoctoral Researcher in Microbial Genomics at the University of Oxford.

I carried out an evolutionary analysis of over 3500 TB genomes to identify novel genetic variants causing antimicrobial resistance (AMR).



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DATA

Data Scientist: The Sexiest Job of the 21st Century

by Thomas H. Davenport and D.J. Patil

From the October 2012 Issue

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When Jonathan Goldman arrived for work in June 2006 at LinkedIn, the business networking site, the place still felt like a start-up. The company had just under 8 million accounts, and the number was growing quickly as existing members invited their friends and colleagues to join. But users weren't seeking out connections with the people who were already on the site at the rate executives had expected. Something was apparently missing in the social experience. As one LinkedIn manager put it, "It was like arriving at a conference reception and realizing you don't know anyone. So you just stand in the corner sipping your drink—and you probably leave early."

WHAT TO READ NEXT



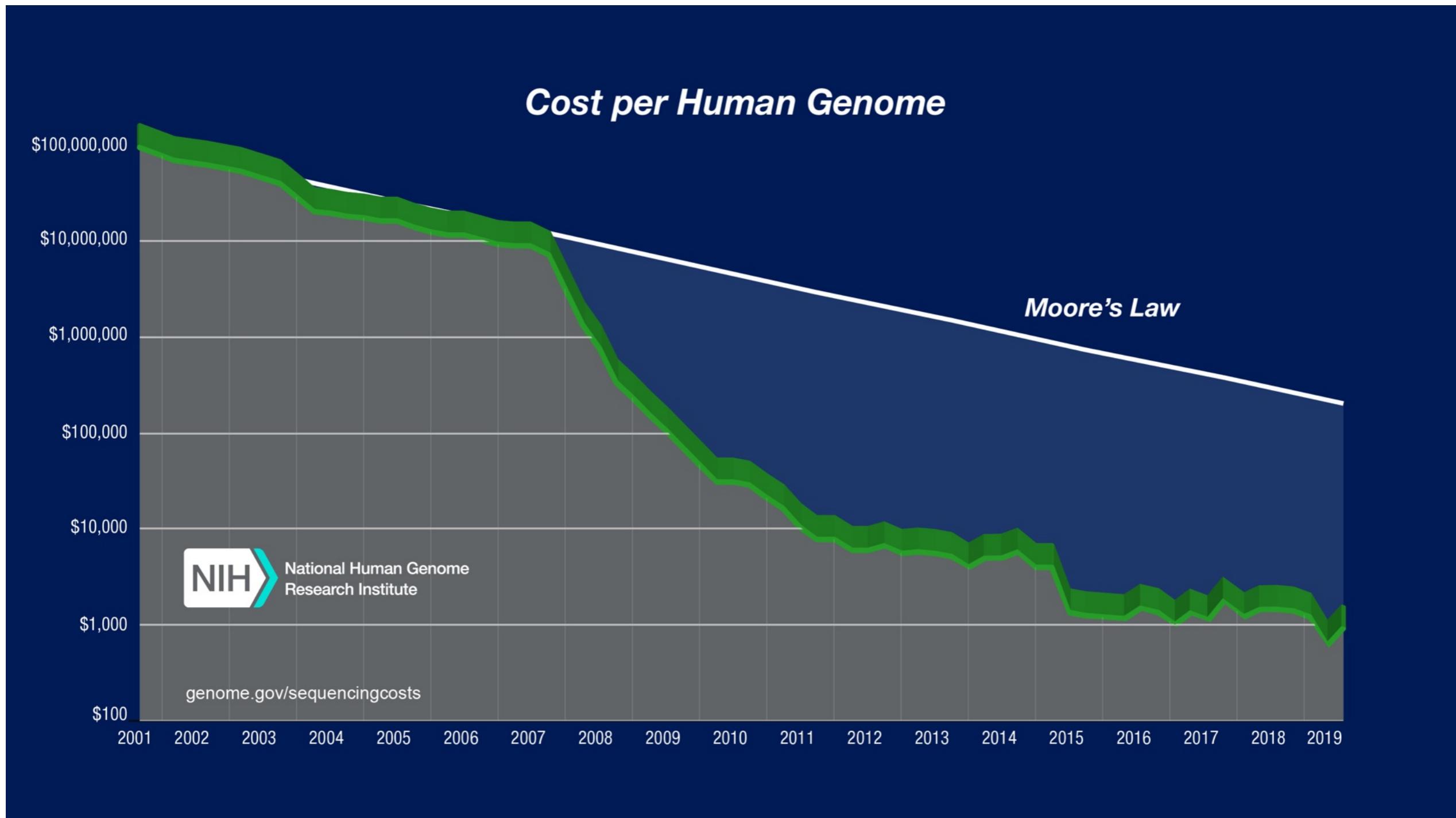
What Data Scientists Really Do, According to 35 Data Scientists

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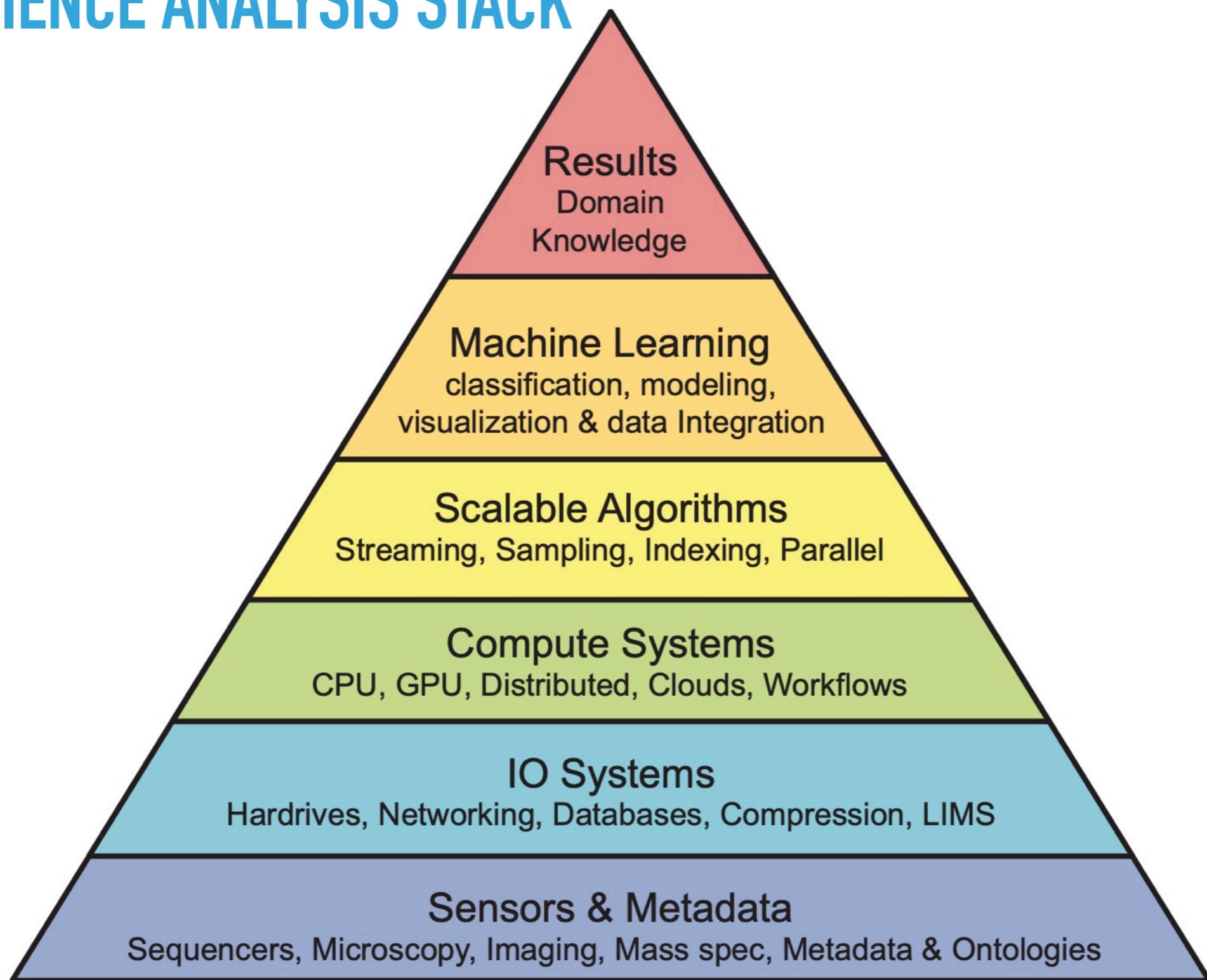
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COST PER GENOME DATA - 2019



<https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data>

DATA SCIENCE ANALYSIS STACK



R IS COMING . . . 😊 😨

The New York Times

Business Computing

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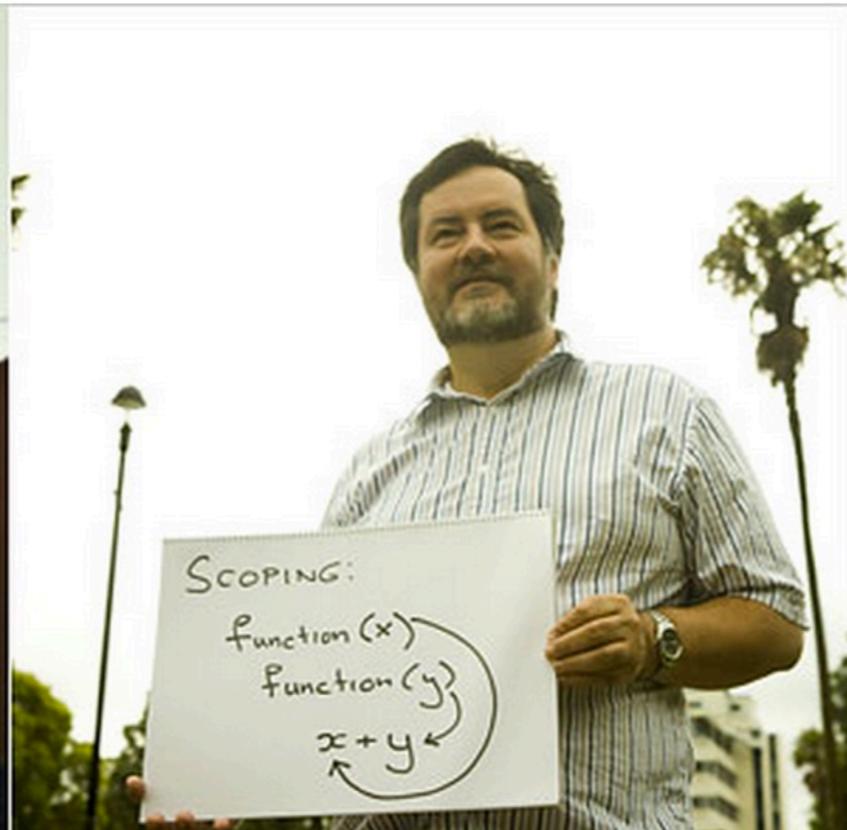
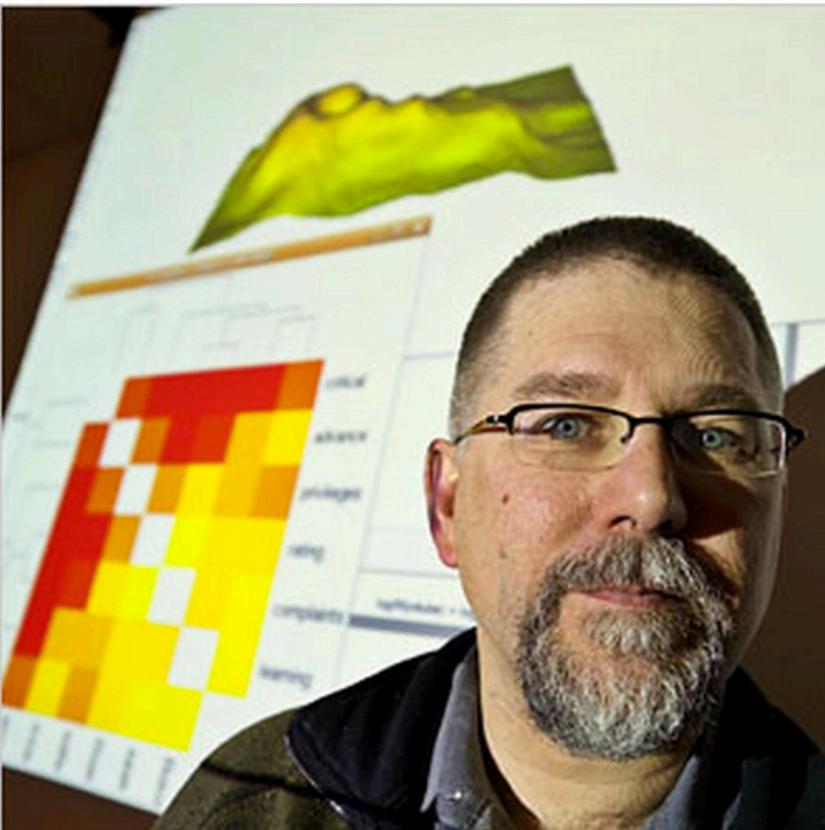
PROGRESS IS EVERYONE'S BUSINESS

See how Goldman Sachs has helped Hologic enable better outcomes for patients.

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Goldman
Sachs

Data Analysts Captivated by R's Power



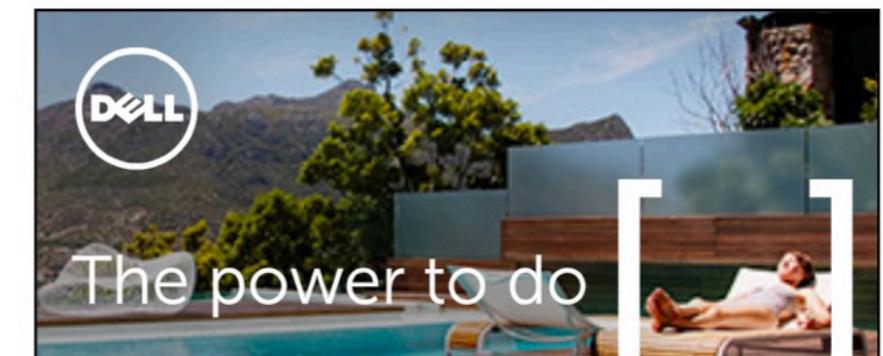
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What's Popular Now

Amiri Baraka,
Polarizing Poet
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Dies at 79



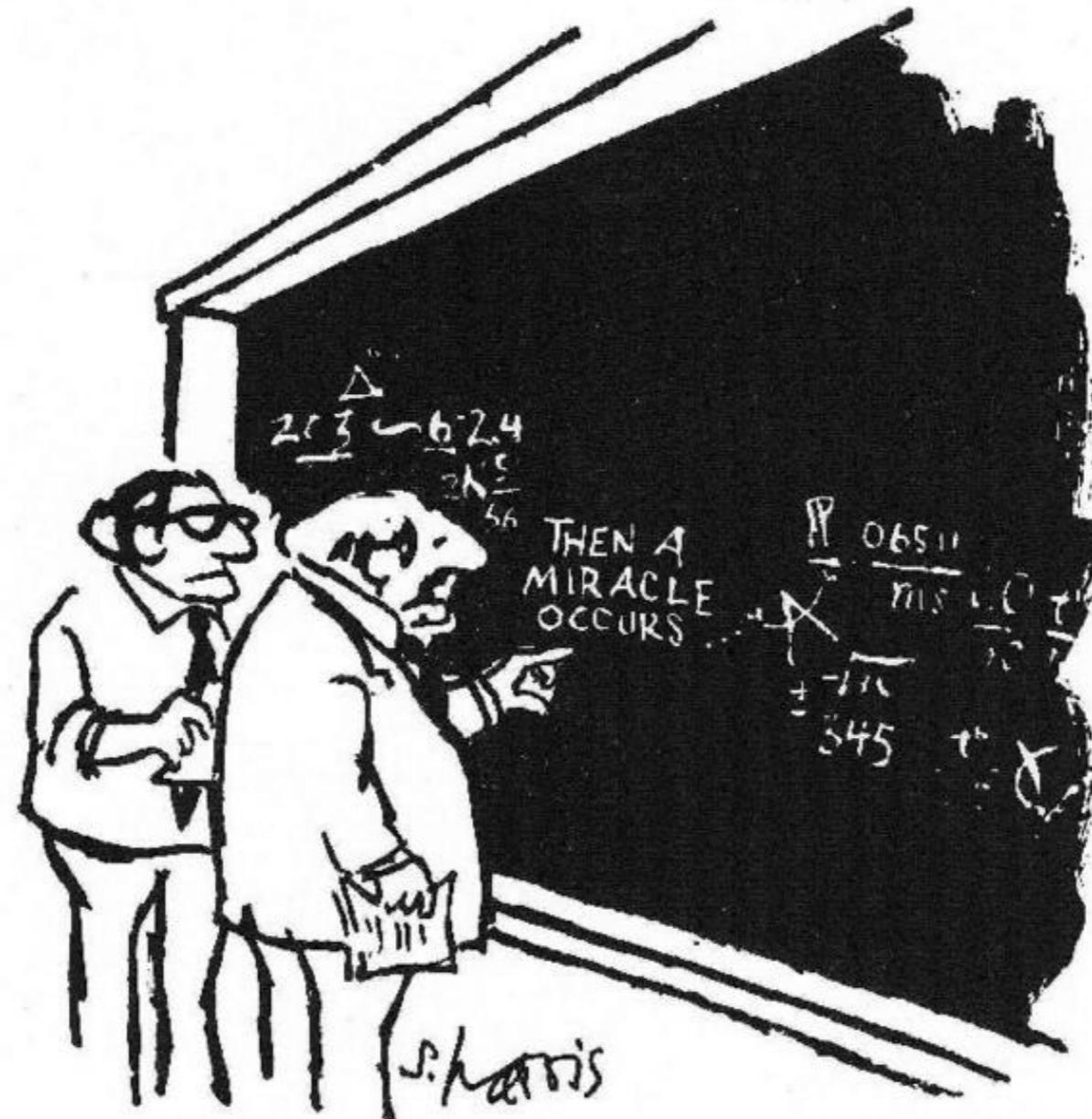
'Very Sad' Chris
Christie Extends
Apology in Bridge
Scandal



R

- ▶ It is free and open source
- ▶ Cross platform: Mac OS, Linux and Windows
- ▶ It has a comprehensive set of packages
- ▶ Thorough documentation
- ▶ R provides a wide variety of statistical (linear and nonlinear modeling, classical statistical tests, time-series analysis, classification, clustering, ...)
- ▶ Graphical techniques, and is highly extensible.

R CAN FACILITATE REPRODUCIBLE RESEARCH



"I think you should be more explicit here in step two."

R CAN FACILITATE REPRODUCIBLE RESEARCH

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RESEARCH

75 COMMENTS

How Bright Promise in Cancer Testing Fell Apart

By GINA KOLATA JULY 7, 2011

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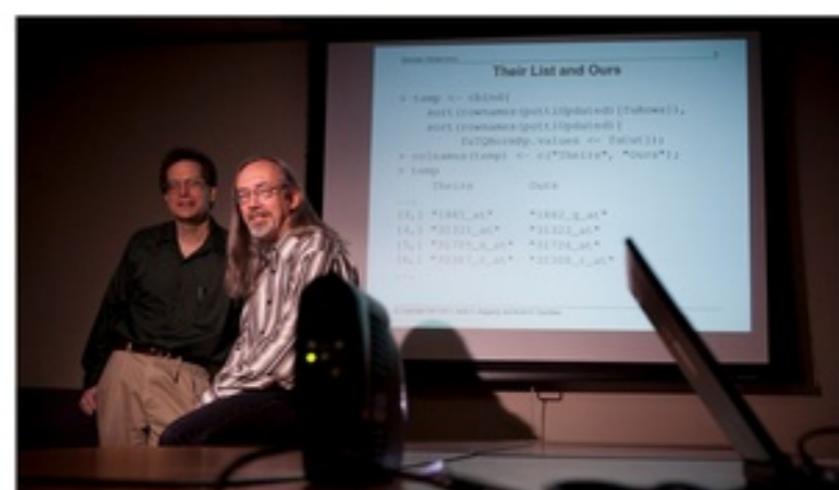
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When Juliet Jacobs found out she had lung [cancer](#), she was terrified, but realized that her hope lay in getting the best treatment medicine could offer. So she got a second opinion, then a third. In February of 2010, she ended up at [Duke University](#), where she entered a research study whose promise seemed stunning.

Doctors would assess her [tumor](#) cells, looking for gene patterns that would determine which [drugs](#) would best



Keith Baggerly, left, and Kevin Coombes, statisticians at M. D. Anderson Cancer Center, found flaws in research on tumors.

Michael Stravato for The New York Times

TOOLBOX

TIPS FOR OPEN-SOURCE SOFTWARE SUPPORT

Releasing lab-built open-source software often involves a mountain of unforeseen work for the developers.

ILLUSTRATION BY THE PROJECT TWINS



BY ANNA NOWOGRODZKI

On 10 April, astrophysicists announced that they had captured the first ever image of a black hole. This was exhilarating news, but none of the giddy headlines mentioned that the image would have been impossible without open-source software. The image was created using Matplotlib, a Python library for graphing data, as well as other components of the open-source Python ecosystem. Just five days later, the US National Science

Foundation (NSF) rejected a grant proposal to support that ecosystem, saying that the software lacked sufficient impact.

It's a familiar problem: open-source software is widely acknowledged as crucially important in science, yet it is funded nonsustainably. Support work is often handled ad hoc by overworked graduate students and postdocs, and can lead to burnout. "It's sort of the difference between having insurance and having a GoFundMe when their grandma goes to the hospital," says Anne Carpenter, a

computational biologist at the Broad Institute of Harvard and MIT in Cambridge, Massachusetts, whose lab developed the image-analysis tool CellProfiler. "It's just not a nice way to live."

Scientists writing open-source software often lack formal training in software engineering, which means that they might never have learnt best practices for code documentation and testing. But poorly maintained software can waste time and effort, and hinder reproducibility. Biologists who use computational tools routinely spend "hours and hours" trying to ►

On 10 April, astrophysicists announced that they had captured the first ever image of a black hole.

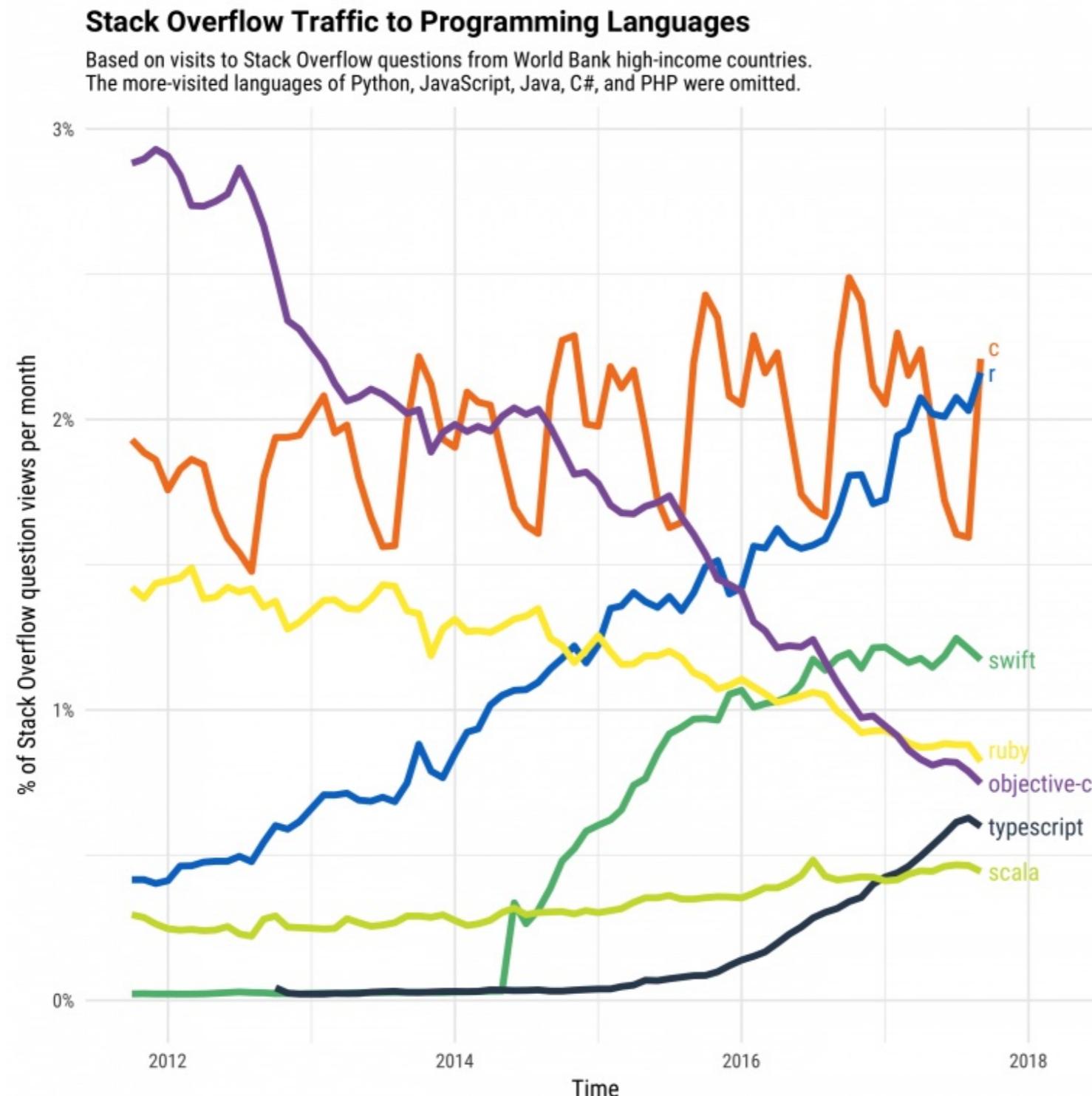
The image was created using Matplotlib, a Python library for graphing data, as well as other components of the open-source Python ecosystem.

If your research group is planning to release open-source software, you can prepare for the support work and the questions that will arise as others begin to use it.

It isn't easy, but the effort can yield citations and name recognition for the developers, and improve efficiency in the field, says Wolfgang Huber, a computational biologist at the European Molecular Biology Laboratory in Heidelberg, Germany. Plus, he adds, "I think it's fun."

Huber also recommends releasing your software to a repository such as the Comprehensive R Archive Network (CRAN) or Bioconductor, an umbrella archive for biological software written in R, instead of to your personal home page or GitHub.

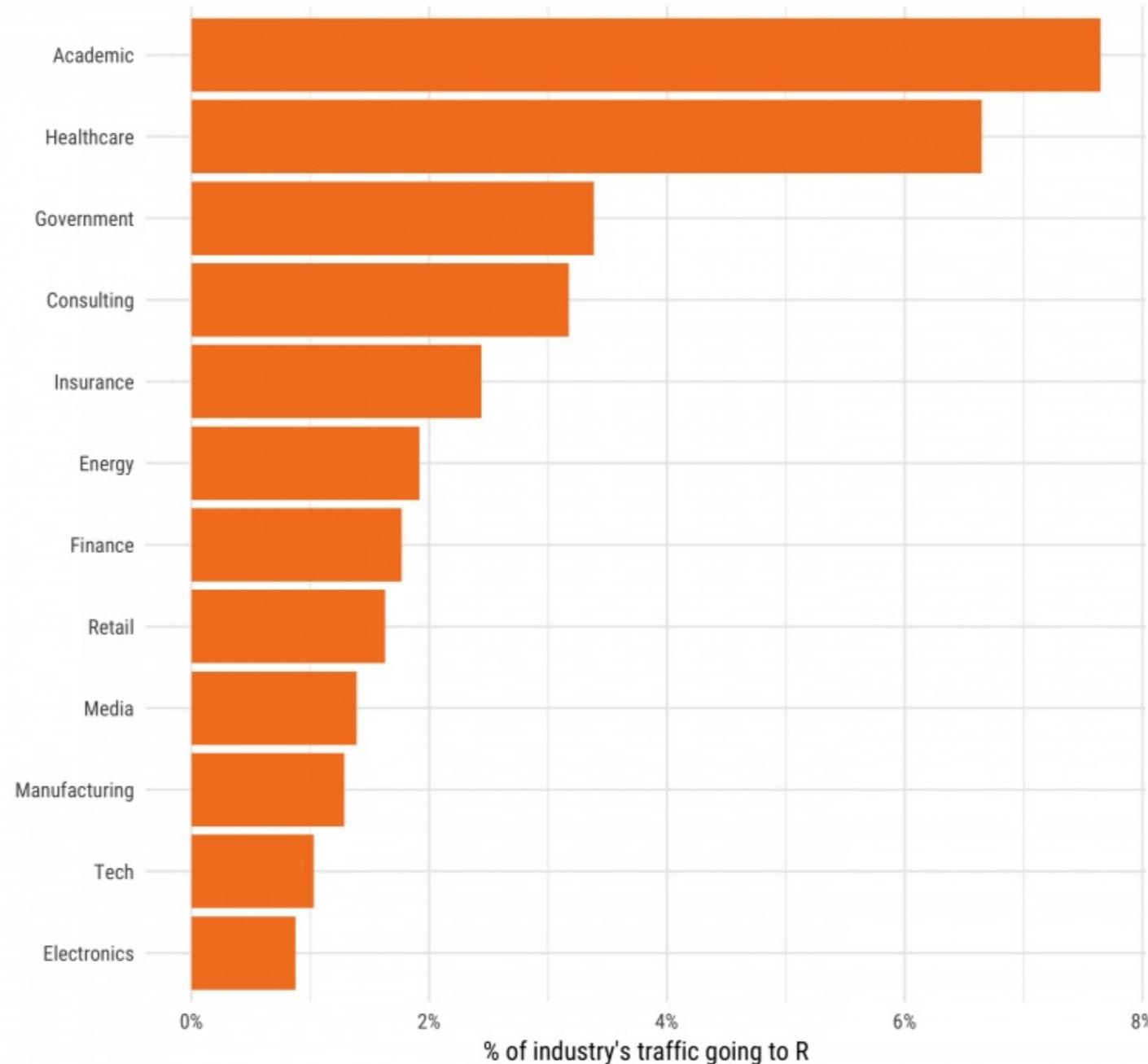
R IS GROWING AT A SIMILAR RATE TO PYTHON



BY INDUSTRY

Visits to R by industry

Based on visits to Stack Overflow questions from the US/UK in January-August 2017.
The denominator in each is the total traffic from that industry.



MANUALS



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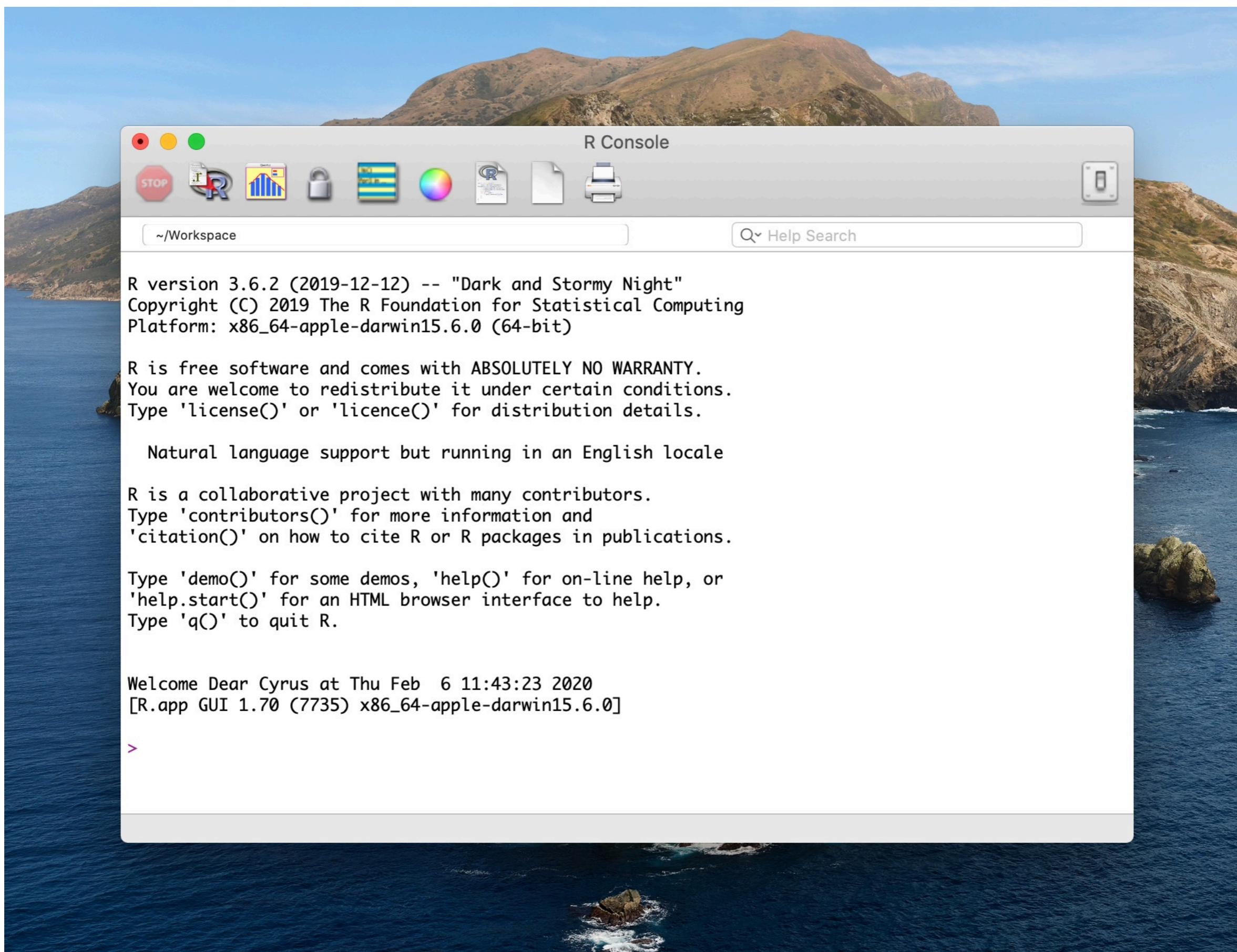
The R Manuals

edited by the R Development Core Team.

The following manuals for R were created on Debian Linux and may differ from the manuals for Mac or Windows on platform-specific pages, but most parts will be identical for all platforms. The correct version of the manuals for each platform are part of the respective R installations. The manuals change with R, hence we provide versions for the most recent released R version (R-release), a very current version for the patched release version (R-patched) and finally a version for the forthcoming R version that is still in development (R-devel).

Here they can be downloaded as PDF files, EPUB files, or directly browsed as HTML:

	Manual	R-release	R-patched	R-devel
	An Introduction to R is based on the former "Notes on R", gives an introduction to the language and how to use R for doing statistical analysis and graphics.	HTML PDF EPUB	HTML PDF EPUB	HTML PDF EPUB
	R Data Import/Export describes the import and export facilities available either in R itself or via packages which are available from CRAN.	HTML PDF EPUB	HTML PDF EPUB	HTML PDF EPUB
	R Installation and Administration	HTML PDF EPUB	HTML PDF EPUB	HTML PDF EPUB
	Writing R Extensions covers how to create your own packages, write R help files, and the foreign language (C, C++, Fortran, ...) interfaces.	HTML PDF EPUB	HTML PDF EPUB	HTML PDF EPUB



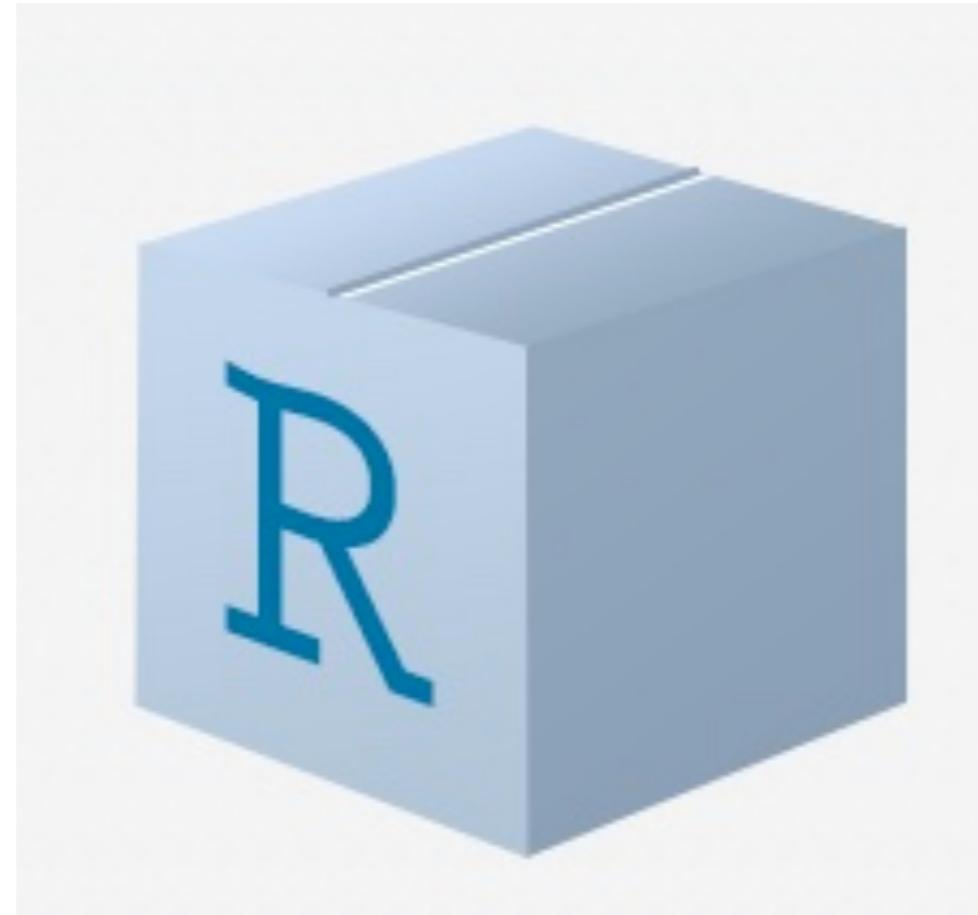
HELLO WORLD!

```
> print("Hello World!")
[1] "Hello World!"
> "Hello World!"
[1] "Hello World!"
```

ARITHMETIC

```
> 2 + 1
[1] 3
> sqrt(36)
[1] 6
> pi
[1] 3.141593
> log(2.718282)
[1] 1
> exp(1)
[1] 2.718282
> 10:20
[1] 10 11 12 13 14 15 16 17 18 19 20
> x <- rnorm(n = 10, mean = 15, sd = 1)
> x
[1] 16.10462 16.48251 13.04309 13.99281 14.88135 14.96106 14.16156
[8] 15.44532 15.93249 14.88073
> mean(x)
[1] 14.98855
> sd(x)
[1] 1.057318
```

PACKAGES



Don't worry, it is not the Schrödinger's cat 😊



- ▶ CODE (R/)
- ▶ PACKAGE METADATA (DESCRIPTION)
- ▶ OBJECT DOCUMENTATION (MAN/)
- ▶ VIGNETTES (VIGNETTES/)
- ▶ TESTING (TESTS/)
- ▶ NAMESPACES (NAMESPACE)
- ▶ DATA (DATA/)
- ▶ COMPILED CODE (SRC/)
- ▶ INSTALLED FILES (INST/)
- ▶ OTHER COMPONENTS

PACKAGE COMPONENTS

The screenshot shows the RDocumentation homepage with a teal background. At the top, there's a navigation bar with links for "R Documentation", "R Enterprise Training", "R package", "Leaderboard", and "Sign in". A large search bar is centered, with the placeholder "Search for packages, functions, e..." and a yellow "Search" button. Below the search bar, text encourages exploring "Task Views". Three sections are highlighted: "Top 5 packages", "Top 5 authors", and "Newest packages", each with a list of five items.

Search all 18,930 CRAN, Bioconductor and GitHub packages.

Search for packages, functions, e... **Search**

Or explore packages in one of the [Task Views](#).

Top 5 packages

Top 5 authors

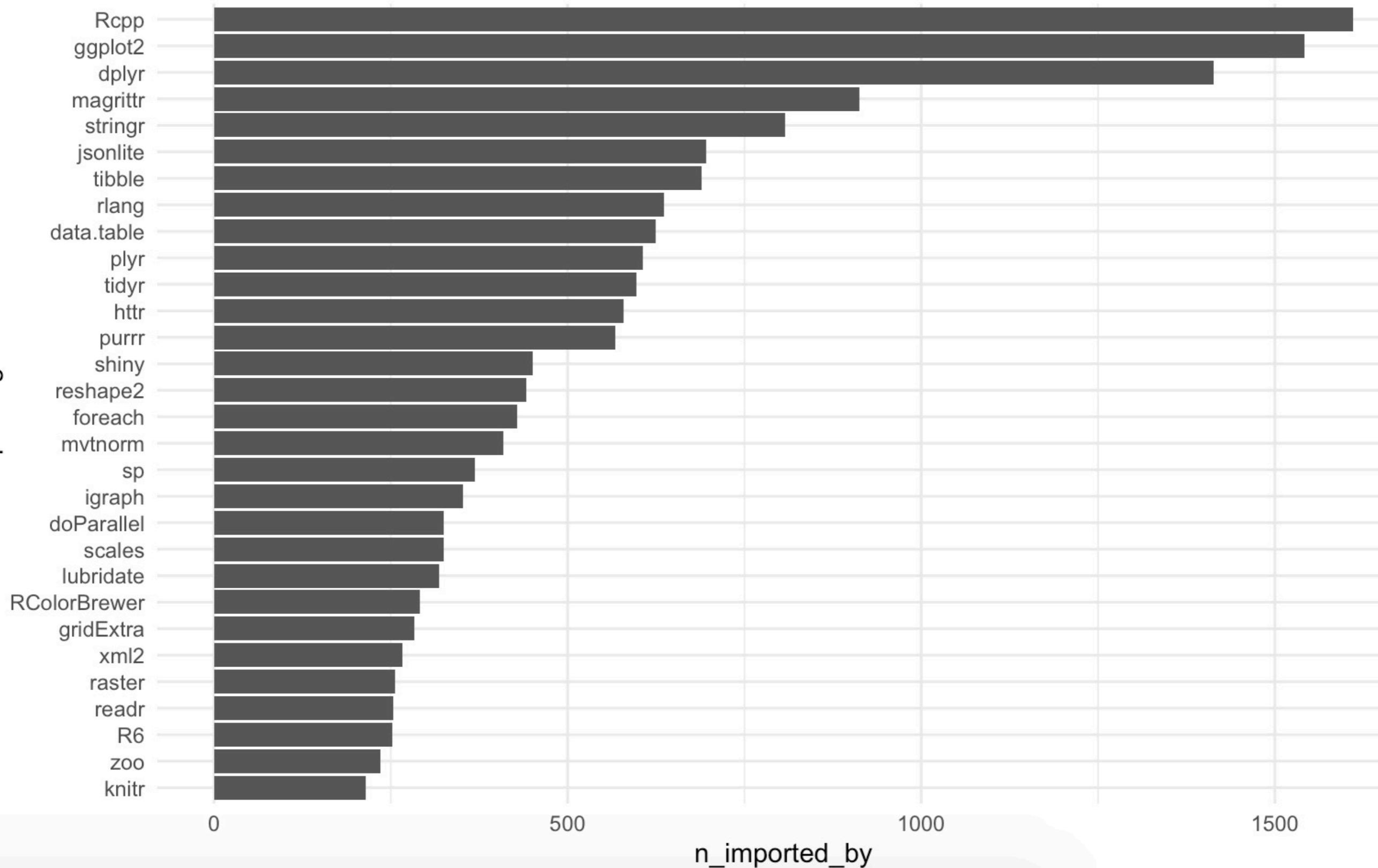
Newest packages

- 1. rpubs
- 2. allestimates
- 3. shinyNotes
- 4. RSQL
- 5. bigsnpr

API documentation Created by [DataCamp.com](#)

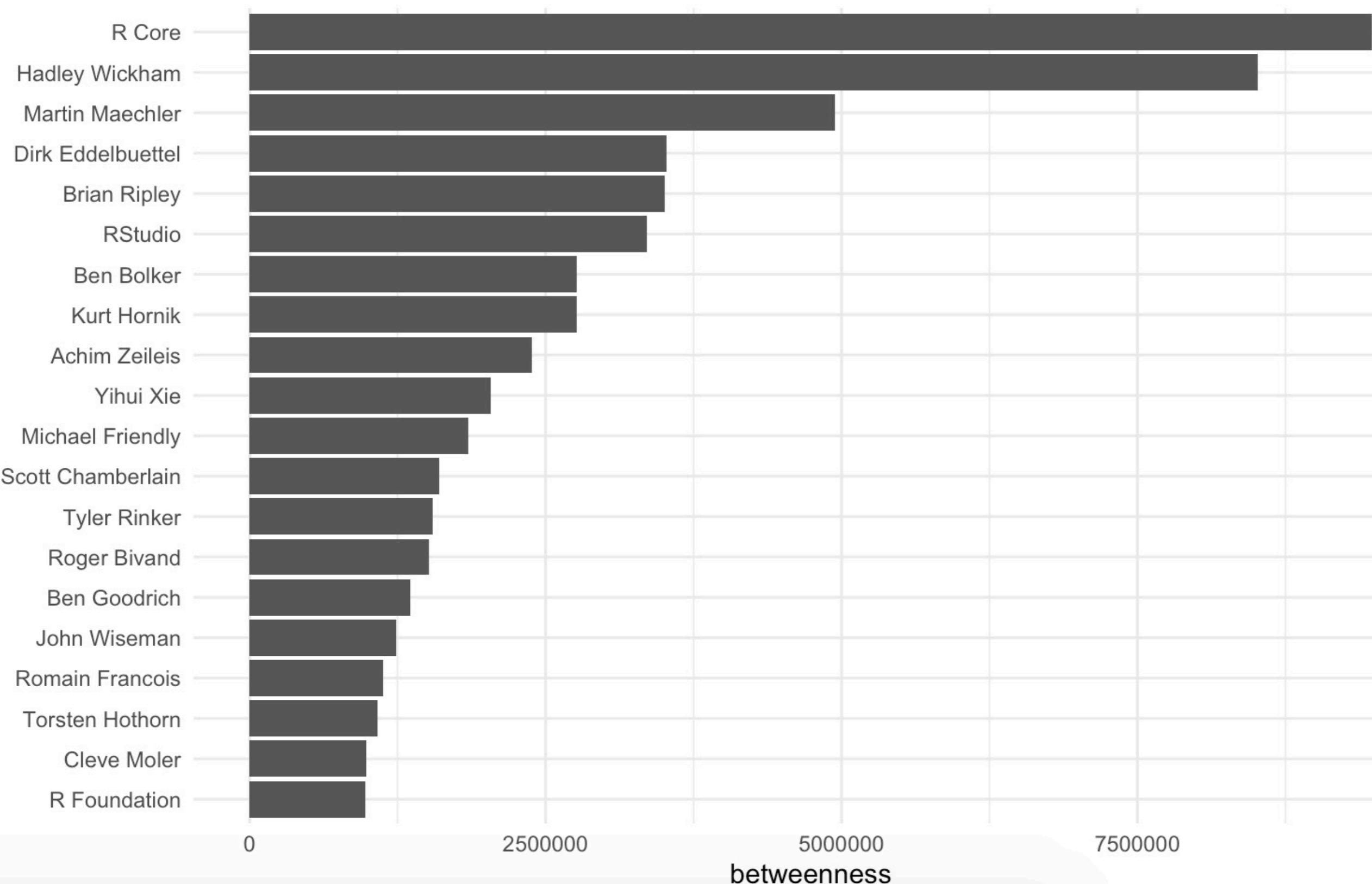
cranly top-30 according to n_imported_by

Package database as of 2020-02-05 20:19:58



cranly top-20 according to betweenness

Package database as of 2020-02-05 20:19:58





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About Bioconductor

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.

Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community.

Bioconductor is also available as an [AMI](#) (Amazon Machine Image) and a series of [Docker](#) images.

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Let's dig in deeper on that

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- ▶ @mortezasabri 
- ▶ @morteza_cyrus_sabri 
- ▶ 09120520015
- ▶ @bioinformatics101 
- ▶ morteza.sabri92@gmail.com



Thank you
for your time



All flower emojis are yours 😊